STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 143390

TO: Phillip Gambel
Location: 3e81 / 3c70
Wednesday, February 02, 2005
Art Unit: 1644
Phone: 272-0844
Serial Number: 08 / 485163

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1a51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

This Page Blank (uspto)

OM nucleic - nucleic search, using sw model

```
                          GenCore version 5.1.6
                          Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:                   January 31, 2005, 21:53:18

                          ; Search time 10474.2 Seconds
                          (without alignments)
                          11205.958 Million cell updates/sec

Title:                    US-08-485-163-4
Perfect score:            2482
Sequence:                 1 CAAGCCCAGAGCCCTGCCAT.........TGAGGGAGGCAGAGTGGGTC 2482

Scoring table:            IDENTITY_NUC
                          Gapop 10.0 , Gapext 1.0
Searched:                 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters:        9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      GenEmbl1:*
                1: gb_ba:*
                2: gb_htg:*
                3: gb_in:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
               10: gb_ro:*
               11: gb_sts:*
               12: gb_sy:*
               13: gb_un:*
               14: gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	2482	100.0	2482	6	AR100741	AR100741 Sequence
2	2482	100.0	2482	6	AR125611	AR125611 Sequence
3	2482	100.0	2482	6	AR130196	AR130196 Sequence
4	2482	100.0	2482	6	AR184212	AR184212 Sequence
5	2482	100.0	2482	6	AR229602	AR229602 Sequence
6	1795	72.3	2009	9	HUMIGCD1	J00230 Human Ig ge
7	1793.4	72.3	2010	9	AF449616	AF449616 Homo sapi
8	1791.8	72.2	2010	9	AF449618	AF449618 Homo sapi
9	1791.8	72.1	2010	9	AF449617	AF449617 Homo sapi
10	1790.2	72.1	56310	2	AC084717	AC084717 Homo sapi
11	1785.4	71.9	176237	9	AC084717	AC084717 Homo sapi
12	1778	71.6	2010	9	AJ928742	AJ928742 Human chr
13	1775.8	71.5	2010	9	AJ250170	AJ250170 Homo sapi
14	1692.8	68.2	10785	6	AR367391	AR367391 Sequence
15	1641.2	66.1	4694	6	AX088865	AX088865 Sequence
16	1635.8	65.9	169802	9	AX478055	AX478055 Sequence
17	1627	65.6	3282	6	AL122127	AL122127 Human chr
18	1627	65.6	3282	6	AR038306	AR038306 Sequence
19	1627	65.6	3282	6	I58595	I58595 Sequence 15
20	1627	65.6	3282	6	I58609	I58609 Sequence 16
21	1627	65.6	13254	6	AR038307	AR038307 Sequence
22	1627	65.6	13254	6	AR038321	AR038321 Sequence
23	1627	65.6	13254	6	I58596	I58596 Sequence 15
24	1627	65.6	13254	6	I58610	I58610 Sequence 17
25	1626.2	65.5	2802	9	HSIGG1CP	Z17370 H.sapiens g
26	1626.2	65.5	4367	6	AX777471	AX777471 Sequence
27	1626.2	65.5	4723	6	AR161379	AR161379 Sequence
28	1626.2	65.5	4723	6	AR369972	AR369972 Sequence
29	1626.2	65.5	4723	6	AX088864	AX088864 Sequence
30	1626.2	65.6	4723	6	AX478054	AX478054 Sequence
31	1626.2	65.5	4723	6	BD096606	BD096606 Transgeni
32	1624.8	65.5	4926	6	AR161427	AR161427 Sequence
33	1624.8	65.5	4926	6	AR370022	AR370022 Sequence
34	1624.8	65.5	4926	6	BD096656	BD096656 Transgeni
35	1624	65.4	8690	6	BD021874	BD021874 Method fo
36	1622.4	65.4	8691	6	BD021861	BD021861 Method fo
37	1621.6	65.3	8614	6	AR176314	AR176314 Sequence
38	1621.6	65.3	8614	6	BD131045	BD131045 Antibody
39	1621.6	65.3	8614	6	AR216773	AR216773 Sequence
40	1621.2	65.3	7874	6	BD021875	BD021875 Method fo
41	1617.2	65.2	2028	9	HUMIGCD2	K01316 Human Ig ge
42	1617.2	65.2	2029	6	AR035227	AR035227 Sequence
43	1617.2	65.2	2029	6	BD182702	BD182702 ANTI-CD4
44	1617.2	65.2	2399	6	AR264654	AR264654 Sequence
45	1617.2	65.2	2560	6	AR035228	AR035228 Sequence

ALIGNMENTS

```
RESULT 1
AR100741

LOCUS       AR100741              2482 bp    DNA       linear   PAT 14-FEB-2001
DEFINITION  Sequence 3 from patent US 6083478.
ACCESSION   AR100741
VERSION     AR100741.1  GI:12811539
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2482)
  AUTHORS   Allaway,G.P. and Maddon,P.J.
  TITLE     Non-peptidyl moiety-conjugated CD4-gamma2 and CD4-IgG2
            Immunoconjugates, and uses thereof
  JOURNAL   Patent: US 6083478-A 3 04-JUL-2000;
            Progenics Pharmaceuticals, Inc.
FEATURES             Location/Qualifiers
     source          1..2482
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match             100.0%;  Score 2482;  DB 6;  Length 2482;
Best Local Similarity   100.0%;
Matches 2482;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy          1 CAAGCCCAGAGCCCTGCCATTTTCTAGTGGGCTCAGGTCCCTACTCGTCAGCCCCTTCCTCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAGCCCAGAGCCCTGCCATTTTCTAGTGGGCTCAGGTCCCTACTCGTCAGCCCCTTCCTCC 60

Qy         61 CTCGGCCAAGGCCACAATGAACCGGGGAGTCCCTTTAGGCACTTGGTCTTCTGGTGCTGCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCGGCCAAGGCCACAATGAACCGGGGAGTCCCTTTAGGCACTTGGTCTTCTGGTGCTGCAA 120

Qy        121 CTGGCCGCTCCTCCCAGCAGCCACTCAGGGAAAGGAAGAAGTGGTGTGCTGGGCAAAAGGGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGCCGCTCCTCCCAGCAGCCACTCAGGGAAAGGAAGAAGTGGTGTGCTGGGCAAAAGGGAT 180

Qy        181 ACAGTGGAACTGACCTGTACAGCTTCCCAGAGAGAGAGGAGCATACAAATTCCACTGGAAAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACAGTGGAACTGACCTGTACAGCTTCCCAGAGAGAGAGGAGCATACAAATTCCACTGGAAAAC 240

Qy        241 TCCAACCAAGATAAAGAGATTCTGGGAAAATCAGGGGCTGCTCCTTCTCTTAACTAAAGGTCCATCCAAG 300
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```
Db  241  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    241  TCCAACCAGATAAAGATTCTGGGAAATCAGGGCTTCCTTCTTAAACTAAAGGTCCATCCAAG  300

Qy  301  CTGAATGATGGCGCTGACTCAAGAAGAGAAACTTCCCCTTGATC  360
Db  301  |||||||||||||||||||||||||||||||||||||||||||||
         CTGAATGATGGCGCTGACTCAAGAAGAGAAACTTCCCCTGATC  360

Qy  361  ATCAAGAAATCTTAAGATAGAAGACTCAGATACTTACATCGTGTAAGTGGAGGACCAGAAG  420
Db  361  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    361  ATCAAGAAATCTTAAGATAGAAGACTCAGATACTTACATCGTGTAAGTGGAGGACCAGAAG  420

Qy  421  GAGGAGGTGCAATTGCTAGTTGTTCGGATTGACCAACTCACCACCTGCTTCAG  480
Db  421  |||||||||||||||||||||||||||||||||||||||||||||||||||||
    421  GAGGAGGTGCAATTGCTAGTTGTTCGGATTGACCAACTCACCACCTGCTTCAG  480

Qy  481  GGGCAGAGCCTGACCCTGGAGAGGACCCCCTGGAGGCCCCCTCAGTGCAAATGT  540
Db  481  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
    481  AGGAGTTCCAAGGGGTAAAAACATACAGGGGGGAGAGGACCCCCTCAGTGCAAATGT  540

Qy  541  AGGAGTTCCAAGGGGTAAAAACATACAGGGGGGAGAGGACCCCCTCAGTGCAAATGT  600
Db  541  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    541  CTCCAGGATAGTGGCACCTGGACATGCACACTGTCTTCTCCAGTCCAGTGGGAGTTC  600

Qy  601  CTCCAGGATAGTGGCACCTGGACATGCACACTGTCTTCTCCAGTCCAGTGGGAGTTC  660
Db  601  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    601  AAAATAGACATCGGTGGTGCTAGCTTTCGCCTTCCTCCAAGGTGTCTTCCCCCTG  660

Qy  661  AAAATAGACATCGGTGGTGCTAGCTTTCGCCTTCCTCCAAGGTGTCTTCCCCCTG  720
Db  661  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    661  GCGCCCTGCTCCAGGAGCACCTCCGGAGAGCACAGCGCCCCGCCCCCTGGGCGCT  720

Qy  721  GCGCCCTGCTCCAGGAGCACCTCCGGAGAGCACAGCGCCCCGCCCCCTGGGCGCT  780
Db  721  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    721  TACTTCCCCGAAACCCGTGAGGGTGCGTGGGAACTCAGGGGCCTGAGTGCAC  840
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(Sequence alignment — query (Qy) and database (Db) nucleotide sequences with positions 241–2460)

OM nucleic - nucleic search, using sw model

Run on:　February 1, 2005, 03:40:26 ; Search time 7912.19 Seconds
　　　　　　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　　　　　　　11430.900 Million cell updates/sec

　　　　　　　　　　GenCore version 5.1.6
　　　　　　　　　　Copyright (c) 1993 - 2005 Compugen Ltd.

Title:　　　　US-08-485-163-4
Perfect score:　2482
Sequence:　　1 CAAGCCCAGAGCCCTGCCAT...........TGAGGGAGGCAGAGAGTGGGTC 2482

Scoring table:　IDENTITY_NUC
　　　　　　　　Gapop 10.0 , Gapext 1.0

Searched:　　32822875 seqs, 1821865908 residues
Total number of hits satisfying chosen parameters:　65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
　　　　　　　　　Maximum Match 100%
　　　　　　　　　Listing first 45 summaries

Database :　　EST:*

　　1: gb_est1:*
　　2: gb_est2:*
　　3: gb_htc:*
　　4: gb_est3:*
　　5: gb_est4:*
　　6: gb_est5:*
　　7: gb_est6:*
　　8: gb_gss1:*
　　9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	720.2	29.0	1231	3	CR592363	CR592363 full-leng
2	713.2	28.7	1224	3	CR625121	CR625121 full-leng
3	688.6	27.7	1158	3	CR623267	CR623267 full-leng
4	674.6	27.1	1194	3	CR603811	CR603811 full-leng
5	672.6	27.1	1060	3	CR602446	CR602446 full-leng
6	668.4	26.9	788	5	BX429840	BX429840 full-leng
7	665.6	26.7	1012	3	CR595292	CR595292 full-leng
8	663.6	26.7	1120	3	CR594421	CR594421 full-leng
9	659.4	26.6	805	5	BX429839	BX429839 full-leng
10	655.4	26.4	932	5	BX438745	BX438745 full-leng
11	645.4	26.0	783	6	CD609192	CD609192 5669931J
12	644.4	26.0	904	5	BX351808	BX351808 full-leng
13	643.6	25.9	1113	3	CR611470	CR611470 full-leng
14	643.2	25.9	812	5	BX429780	BX429780 full-leng
15	642.8	25.9	816	4	BI388409	BI388409 603083373
16	640.6	25.8	1097	3	CR590214	CR590214 full-leng
17	640.6	25.8	1097	3	CR590214	CR590214 full-leng
18	635.8	25.6	785	5	BX429838	BX429838 full-leng
19	635.2	25.6	1287	3	CR611016	CR611016 full-leng
20	634.6	25.6	902	3	CR608756	CR608756 full-leng
21	634.6	25.6	918	3	CR597050	CR597050 full-leng
22	634.6	25.6	975	3	CR608814	CR608814 full-leng
23	634.6	25.6	1091	3	CR604840	CR604840 full-leng
24	634.6	25.6	1091	3	CR611575	CR611575 full-leng
25	633.6	25.5	1089	3	CR599517	CR599517 full-leng
26	633.6	25.5	1090	3	CR594433	CR594433 full-leng
27	633.4	25.5	801	4	BI822118	BI822118 603039813
28	632.6	25.5	1089	3	CR604209	CR604209 full-leng
29	632	25.4	822	5	BX457159	BX457159 full-leng
30	631.6	25.4	1136	3	CR598462	CR598462 full-leng
31	629.6	25.4	1086	3	CR603347	CR603347 full-leng
32	629.6	25.4	1086	3	CR606727	CR606727 full-leng
c 33	629	25.3	840	4	BI838893	BI838893 603087279
34	628.6	25.3	1057	3	BX417147	BX417147 full-leng
35	624.2	25.2	1224	3	CR609874	CR609874 full-leng
36	624.2	25.1	1142	3	CR598316	CR598316 full-leng
37	623.2	25.1	1078	5	CR602414	CR602414 full-leng
c 38	622.6	25.1	1039	5	BX355903	BX355903 full-leng
39	622.4	25.1	791	4	BI819727	BI819727 603041415
40	622.4	25.1	845	3	BX367837	BX367837 full-leng
41	620.8	25.0	1120	3	CR619868	CR619868 full-leng
c 42	620.4	25.0	1022	6	BX385912	BX385912 full-leng
c 43	619	24.9	760	6	CA447963	CA447963 UI-H-EI0-
c 44	618.6	24.9	784	5	BQ712730	BQ712730 AGENCOURT
c 45	616.6	24.8	1068	5	BX359678	BX359678 BX359678

ALIGNMENTS

RESULT 1
CR592363
LOCUS　　　　CR592363　　　　　　　　1231 bp　　mRNA　　linear　　HTC 21-JUL-2004
DEFINITION　full-length cDNA clone CS0DE006YK04 of Placenta of Homo sapiens
　　　　　　　(human).
ACCESSION　CR592363
VERSION　　CR592363.1　　GI:50473170
KEYWORDS　HTC; CNSLT_cDNA.
SOURCE　　Homo sapiens (human)
　ORGANISM　Homo sapiens
　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE　1　(bases 1 to 1231)
　AUTHORS　Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
　TITLE　　Full-length cDNA libraries and normalization
　JOURNAL　Unpublished
　REMARK　Contact : Peng Liang Email : fliang@lifetech.com URL :
　　　　　　http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
　　　　　　Faraday Avenue
REFERENCE　2　(bases 1 to 1231)
　AUTHORS　Genoscope.
　TITLE　　Direct Submission
　JOURNAL　Submitted (20-JUL-2004) Genoscope - Centre National de Sequence :
　　　　　　BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
　　　　　　- Web : www.genoscope.cns.fr)
COMMENT　　1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
　　　　　　end enriched, double-strand cDNA was digested with Not I and cloned
　　　　　　into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
　　　　　　was normalized. Library was constructed by Life Technologies, a
　　　　　　division of Invitrogen.
FEATURES　　　　　　　　　Location/Qualifiers
　　　　source　　　　　1..1231
　　　　　　　　　　　　/organism="Homo sapiens"
　　　　　　　　　　　　/mol_type="mRNA"
　　　　　　　　　　　　/db_xref="taxon:9606"
　　　　　　　　　　　　/clone="CS0DE006YK04"
　　　　　　　　　　　　/tissue_type="placenta"
　　　　　　　　　　　　/plasmid="pCMVSPORT_6"
ORIGIN
　Query Match　　29.0%;　　Score 720.2;　DB 3;　Length 1231;
　Best Local Similarity　87.0%;　Pred. No. 4.1e-167;
　Matches　857;　Conservative　0;　Mismatches　28;　Indels 100;　Gaps　2;

Qy　　1395 TGCCCACCGGTGCCCAGGTAAGCCAGCCAGCCGCCCTCGCCCTTCAGCTCAAGGCGGGACAGG 1454
　　　　　　 |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db　　 344 TGCCCACCCATGTGCCAAGTAAGCCAGCCCAGCCCCAGGCCTGCCTTCGCCTCCAGCTCAAGGCCGCGGGACAGG 403

KEYWORDS   HTC; CNSIT_cDNA.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1224)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK   Contact: Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2 (bases 1 to 1224)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (20-JUL-2004). Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
     source   1..1224
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI015YH20"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Query Match   28.7%;   Score 713.2; DB 3; Length 1224;
Best Local Similarity   86.9%;   Pred. No. 2.2e-165;
Matches 850;   Conservative   0;   Mismatches   28;   Indels 100;   Gaps 2;

RESULT 2
LOCUS   CR625121   1224 bp   mRNA   linear   HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI015YH20 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR625121
VERSION   CR625121.1 GI:5050928

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6

Run on: February 1, 2005, 00:31:21 ; Search time 1195.54 Seconds
(without alignments)
10898.026 Million cell updates/sec

Title: US-08-485-163-4
Perfect score: 2482
Sequence: 1 CAAGCCCAGAGCCCTGCCAT.............TGAGGGAGGCAGAGTGGGTC 2482

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   N_Geneseq 23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2482	100.0	2482	2	AAQ28089	Aaq28089 Encodes C
2	2482	100.0	2482	2	AAZ98856	Aaz98856 CD4-IgG2
3	2482	100.0	2482	4	AAF56396	Aaf56396 CD4-IgG2
4	2482	100.0	2482	4	AAF77830	Aaf77830 Coding se
5	2482	100.0	2482	10	ABS55721	Abs55721 DNA encod
6	2482	100.0	2482	11	ADM18321	Adm18321 Human CD4
7	2472.4	99.6	2482	2	AAQ57751	Aaq57751 CD4-IgG2
8	2261.6	91.1	2488	2	AAQ27831	Aaq27831 Sequence
9	2158.4	87.0	11228	10	ACH00964	Ach00964 Pro 542 a
10	1795	72.3	2009	10	ADE97377	Ade97377 Human IgG
11	1692.8	68.2	10704	2	AAQ43846	Aaq43846 Plasmid p
12	1641.2	66.1	4694	4	AAF55225	Aaf55225 Nucleotid
13	1641.2	66.1	4694	6	ABK85577	Abk85577 Human IgG
14	1627	65.6	3282	6	AAT40914	Aat40914 DNA encod
15	1627	65.6	3282	10	ADE06733	Ade06733 Human IgG
16	1627	65.6	3282	2	AAT40915	Aat40915 Nucleotid
17	1627	65.6	13254	3	AAA32165	Aaa32165 Complete
18	1626.2	65.5	13254	8	ACC47228	Acc47228 Hu266 N56
19	1626.2	65.5	3223	8	AAS11982	Aas11982 DNA encod
20	1626.2	65.5	3223	8	ACC47227	Acc47227 Hu266 N56
21	1626.2	65.5	3244	8	ABZ24635	Abz24635 Humanised
22	1626.2	65.5	3256	10	ABZ24641	Abz24641 Humanised
23	1626.2	65.5	4367	10	ADD13789	Add13789 Plasmid p
24	1626.2	65.5	4723	2	AAT78802	Aat78802 Gamma hea
25	1626.2	65.5	4723	2	AAV39243	Aav39243 Plasmid p
26	1626.2	65.5	4723	2	AAZ21997	Aaz21997 Nucleotid
27	1626.2	65.5	4723	4	AAF55224	Aaf55224 Nucleotid
28	1625.4	65.5	4723	6	ABK85576	Abk85576 Human IgG
29	1625.4	65.5	3282	3	AAA31025	Aaa31025 B12 IgG1
30	1625.4	65.5	7073	2	AAT50962	Aat50962 TF8-5G9 C
31	1625.4	65.5	13254	3	AAA32045	Aaa32045 pEe12 Com
32	1624.8	65.5	4926	2	AAV39291	Aav39291 Plasmid p
33	1624.8	65.5	4926	3	AAA32164	Aaa32164 B12 IgG2
34	1624.6	65.4	13254	3	AAA32045	Aaa32045 Nucleotid
35	1624.4	65.4	3282	3	ADN61720	Adn61720 DNA encod
36	1623.8	65.4	3282	3	AAA32151	Aaa32151 pEe12 Com
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41	1619.8	65.3	9201	2	AAZ10201	Aaz10201 Expressio
42	1619	65.2	3282	2	AAH43776	Aah43776 Chi220 he
43	1618	65.2	7874	2	AAZ10201	Aaz10201 Expressio
44	1617.4	65.2	13254	3	AAA55003	Aaa55003 Humanised
45	1617.2	65.2	2028	10	AAA31038	Aaa31038 Humanised

ALIGNMENTS

RESULT 1
AAQ28089
ID   AAQ28089 standard; cDNA; 2482 BP.
XX
AC   AAQ28089;
XX
DT   24-OCT-2003 (revised)
DT   25-MAR-2003 (revised)
DT   06-FEB-1993 (first entry)
XX
DE   Encodes CD4-IgG2 chimeric heavy chain.
XX
KW   homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW   chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key   Location/Qualifiers
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FT   CDS   76..980
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FT   CDS   688..981
FT   /label= CD4 domain
FT   /*tag= e
FT   CDS   1374..1408
FT   /label= CH1 domain
FT   /*tag= b
FT   CDS   1528..1854
FT   /label= hinge domain
FT   /*tag= c
FT   CDS   1976..2275
FT   /label= CH2 domain
FT   /*tag= d
FT   CDS
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PN   WO9213947-A1.
XX
PD   20-AUG-1992.
XX
PF   10-FEB-1992; 92WO-US001143.
XX
PR   08-FEB-1991; 91US-00653684.
XX
PA   (PROG-) PROGENICS PHARM INC.

XX
PI   Beaudry GA, Maddon PJ;
XX
DR   WPI; 1992-300034/36.
DR   P-PSDB; AAR26783.
XX
PT   CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT   treatment, prevention and diagnosis of HIV infection.
XX
PS   Claim 13; Fig 4; 90pp; English.
XX
CC   This sequence encodes a CD4-gamma2 chimeric heavy chain homodimer. Human
CC   CD4 cDNA was excised from plasmid pSP6T4 as an EcoRI/StuI 0.7 kb
CC   fragment, and cloned into M13mp18 forming M13mp18(CD4). This was
CC   linearised with PstI, and the SacII(flush)/PstI fragment from pBr gamma2
CC   containing human gamma2 heavy chain (CH1 exon) isolated and ligated to
CC   the M13mp18(CD4) vector. Resulting recombinants were then screened by
CC   restriction analysis for the presence of both CD4 and CH1 which occur in
CC   tandem CD4(EcoRI/StuI)-CH1(SacI(flush)/PstI). Site directed mutagenesis
CC   was performed to juxtapose the CD4 and CH1 heavy chain sequences in
CC   frame. The resulting chimeric DNA molecule encodes a protein containing
CC   the V1V2 domains of CD4 fused to the CH1 domain of heavy chain. Plaques
CC   containing the chimeric gene with the correct sequence were then grown in
CC   TG1 cells and Rf DNA isolated from the cells. (Updated on 25-MAR-2003 to
CC   correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 2482 BP; 559 A; 812 C; 676 G; 435 T; 0 U; 0 Other;

Query Match   100.0%; Score 2482; DB 2; Length 2482;
Best Local Similarity 100.0%; Pred. No.0;
Matches 2482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 CAAGCCCAGAGCCCTGCACCATTTCTGTGGGGCTTCAGGTTCCCTACTGCTTCAGCGCCCTTCCTCC    60

Qy     61 CTCGGCAAGGCCACAATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGTGCAA          120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTCGGCAAGGCCACAATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGTGCAA          120

Qy    121 CTGGGCGCCTTCCTCCCAGCAGCACTCAGGGGAAGAAGAAAGTGGTGGCTGCGGCAAAAAAGGGGAT    180
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Qy    181 ACAGTGGGAACTGACCTGTACAGCTTCCCAGAAGAAGAGCATACAAATTCCACTGGAAAAAC        240
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Qy    241 TCCAACCAGATAAAAGATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTGGTCCATCCAAG     300
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Qy    301 CTGAATGATCGCGCTGACTCAAGAGAAGAAGCCTTTGGACCAAGGAAACTTCCCCTGATC        360
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Db    301 CTGAATGATCGCGCTGACTCAAGAGAAGAAGCCTTTGGACCAAGGAAACTTCCCCTGATC        360

Qy    361 ATCAAGAATCTTAAGATGAAGAACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAG     420
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Qy    601 CTCCAGGATAGTGGGCACCTGGACATGCACTGTCTTGCGAAGAAGGTGGAGTTC         660
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Qy    601 CTCCAGGATAGTGGGCACCTGGACATGCACTGTCTTGCGAAGAAGGTGGAGTTC         660
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: February 1, 2005, 09:02:41 ; Search time 1340.46 seconds
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Perfect score: 2482
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Scoring table: IDENTITY_NUC
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Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2482	100.0	2482	8	US-08-485-163-4	Sequence 4, Appli
2	2482	100.0	2482	9	US-09-766-995-3	Sequence 3, Appli
3	2158.4	87.0	11228	16	US-10-397-569-6	Sequence 6, Appli
4	1795	72.3	2009	13	US-10-047-542-55	Sequence 55, Appl
5	1795	72.3	2009	18	US-10-756-153-31	Sequence 31, Appl
6	1641.2	66.1	4694	9	US-09-948-939-41	Sequence 41, Appl
7	1641.2	66.1	4694	13	US-10-047-542-55	Sequence 3, Appli
8	1627	65.6	3282	15	US-10-016-986-154	Sequence 154, App
9	1627	65.6	3282	15	US-10-016-986-169	Sequence 169, App
10	1627	65.6	3282	15	US-10-410-907A-3	Sequence 3, Appli
11	1627	65.6	13254	15	US-10-016-986-156	Sequence 156, App
12	1627	65.6	13254	15	US-10-016-986-170	Sequence 170, App

ALIGNMENTS

13	1626.2	65.5	4723	9	US-09-948-939-40	Sequence 2, Appl
14	1626.2	65.5	4723	13	US-10-000-433-2	Sequence 2, Appli
15	1617.2	65.2	2028	13	US-10-047-542-57	Sequence 57, Appl
16	1617.2	65.2	2399	15	US-10-267-286A-1	Sequence 1, Appl
17	1611.8	64.9	8687	16	US-10-467-546-15	Sequence 15, Appl
18	1611.8	64.9	8687	16	US-10-467-546-16	Sequence 16, Appl
19	1584.6	63.8	2249	9	US-09-249-011A-23	Sequence 23, Appl
20	1584.4	63.8	2011	17	US-10-684-109-80	Sequence 80, Appl
21	1584.4	63.8	2011	17	US-10-684-109-81	Sequence 81, Appl
c 22	1582.6	63.8	1990	17	US-10-684-109-69	Sequence 69, Appl
c 23	1582.6	63.8	1990	17	US-10-684-109-70	Sequence 70, Appl
c 24	1582	63.7	1990	17	US-10-684-109-86	Sequence 86, Appl
c 25	1582	63.7	1990	17	US-10-684-109-87	Sequence 87, Appl
c 26	1582	63.7	1990	17	US-10-684-109-98	Sequence 98, Appl
c 27	1582	63.7	1990	17	US-10-684-109-99	Sequence 99, Appl
28	1582	63.7	1990	17	US-10-684-109-104	Sequence 104, App
29	1582	63.7	1990	17	US-10-684-109-105	Sequence 105, App
c 30	1582	63.7	1996	17	US-10-684-109-92	Sequence 92, Appl
c 31	1582	63.7	1996	17	US-10-684-109-93	Sequence 93, Appl
32	1582	63.7	1996	17	US-10-684-109-110	Sequence 110, App
c 33	1582	63.7	1996	17	US-10-684-109-111	Sequence 111, App
34	1581.8	63.7	1999	14	US-10-153-382-2	Sequence 2, Appli
35	1581.8	63.7	1999	18	US-10-612-497-54	Sequence 54, Appl
36	1581.8	63.7	1999	18	US-10-776-649-54	Sequence 54, Appl
37	1574.6	63.4	2009	13	US-10-047-542-54	Sequence 54, Appl
38	1574.6	63.4	2009	13	US-10-257-907-4	Sequence 4, Appli
39	1574.6	63.4	2770	13	US-10-027-075-29	Sequence 29, Appl
40	1574.6	63.4	2770	17	US-10-792-637-29	Sequence 29, Appl
41	1574.6	63.4	2160	16	US-10-428-408A-31	Sequence 31, Appl
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44	1454.8	58.6	2071	15	US-10-216-484-116	Sequence 116, App
45	1454.8	58.6	2071	15	US-10-384-933-116	Sequence 116, App

RESULT 1
US-08-485-163-4

; Sequence 4, Application US/08485163
; Publication No. US20020981Al

GENERAL INFORMATION:
  APPLICANT: Beaudry, Gary A.
  APPLICANT: Madden, Paul J.
  TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
  NUMBER OF SEQUENCES: 10
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Cooper & Dunham LLP
    STREET: 1185 Avenue of the Americas
    CITY: New York
    STATE: New York
    COUNTRY: USA
    ZIP: 10036
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.24
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/485,163
    FILING DATE: 07-JUN-1995
    CLASSIFICATION: 514
  ATTORNEY/AGENT INFORMATION:
    NAME: White, John P.
    REGISTRATION NUMBER: 28,678
    REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212) 278-0400
    TELEFAX: (212) 391-0525
    TELEX:
  INFORMATION FOR SEQ ID NO: 4:
    SEQUENCE CHARACTERISTICS:

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;   LENGTH:    2482 base pairs
;   TYPE:      nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY:  unknown
;   MOLECULE TYPE: cDNA
;   ORIGINAL SOURCE:
;     ORGANISM:  homo sapien
;     CELL TYPE: lymphocyte
;   US-08-485-163-4

Query Match            100.0%;   Score 2482;  DB 8;   Length 2482;
Best Local Similarity  100.0%;   Pred. No. 0;
Matches 2482;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy 1741 GTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAG 1800
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Qy 1801 GTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCAAAAACCAAAAGGTGGG 1860
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Qy 1861 ACCCGCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGG 1920
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Qy 1921 AGTGACCGGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACAGGTGTACAC 1980
Db 1921 AGTGACCGGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACAGGTGTACAC 1980

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 03:49:56 ; Search time 211.903 Seconds
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                                               8325.401 Million cell updates/sec

Title: US-08-485-163-4
Perfect score: 2482
Sequence: 1 CAAGCCCAGAGCCCTGCCAT..........TGAGGGAGGCCAGAGTGGGTC 2482

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2482	100.0	2482	3	US-08-477-460B-3	Sequence 3, Appli
2	2482	100.0	2482	3	US-08-379-516-3	Sequence 3, Appli
3	2482	100.0	2482	3	US-09-329-916-3	Sequence 3, Appli
4	2482	100.0	2482	3	US-08-485-372A-3	Sequence 3, Appli
5	2482	100.0	2482	3	US-09-409-006A-3	Sequence 3, Appli
6	2482	100.0	2482	4	US-08-484-681-3	Sequence 3, Appli
7	2482	100.0	2482	3	US-09-766-995-3	Sequence 3, Appli
8	2482	100.0	2482	5	PCT-US93-07422-3	Sequence 3, Appli
9	2482	100.0	2482	3	PCT-US93-07422-3	Sequence 3, Appli
10	1692.8	68.2	10785	3	US-08-444-644-27	Sequence 27, Appl
11	1692.8	68.2	10785	3	US-08-232-246A-27	Sequence 27, Appl
12	1627	65.6	3282	1	US-08-276-852-154	Sequence 154, App
13	1627	65.6	3282	1	US-08-276-852-169	Sequence 169, App
14	1627	65.6	3282	1	US-08-899-575-154	Sequence 154, App
15	1627	65.6	3282	1	US-08-899-575-169	Sequence 169, App
16	1627	65.6	3282	5	PCT-US95-08743-154	Sequence 154, App
17	1627	65.6	3282	5	PCT-US95-08743-169	Sequence 169, App
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19	1627	65.6	13254	1	US-08-276-852-156	Sequence 156, App
20	1627	65.6	13254	1	US-08-276-852-170	Sequence 170, App
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24	1627	65.6	13254	5	PCT-US95-08743-170	Sequence 170, App
25	1627	65.6	13254	5	PCT-US95-08743-156	Sequence 156, App
26	1627	65.6	13254	5	PCT-US95-08743-170	Sequence 170, App
27	1626.2	65.5	4723	3	US-09-042-353-370	Sequence 370, App
28	1626.2	65.5	4723	3	US-08-758-417A-218	Sequence 218, App
29	1624.8	65.5	4926	3	US-09-042-353-418	Sequence 418, App
30	1624.8	65.5	4926	3	US-08-758-417A-268	Sequence 268, App
31	1621.6	65.3	8614	3	US-09-247-352-5	Sequence 5, Appli
32	1621.6	65.3	8614	4	US-09-466-635-5	Sequence 5, Appli
33	1617.2	65.2	2029	2	US-07-916-098A-43	Sequence 43, Appli
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35	1617.2	65.2	2399	4	US-08-557-050-11	Sequence 11, Appl
36	1617.2	65.2	2560	4	US-07-916-098A-44	Sequence 44, Appl
37	1601.4	64.5	2399	4	US-08-444-644-41	Sequence 41, Appl
38	1601.4	64.5	10844	3	US-08-232-246A-41	Sequence 41, Appl
39	1581.8	63.7	10844	3	US-09-472-087-54	Sequence 54, Appl
40	1574.6	63.4	1999	4	US-09-225-595-29	Sequence 29, Appl
41	1574.6	63.4	2770	4	US-08-595-590B-29	Sequence 29, Appl
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43	1570	63.3	2009	1	US-08-444-644-18	Sequence 18, Appl
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45	1495.4	60.2	11528	1	US-08-109-106-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-08-477-460B-3

; Sequence 3, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,460B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2482 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-477-460B-3

Query Match   100.0%; Score 2482; DB 3; Length 2482;
Best Local Similarity   100.0%; Pred. No. 0;

Matches 2482;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Db   1   CAAGCCCAGAGCCCTGCCATTTCTGTGGGTCCAGTTCCTACTGCTTCAGTCTCAGCCCTTCCTCC   60

(Left column: paired Qy / Db alignment rows continuing from position 1 to 1080, in increments of 60)

(Right column: paired Qy / Db alignment rows continuing from position 1081 to 2160, in increments of 60)

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: January 31, 2005, 21:53:18

Title: US-08-485-163-6
Perfect score: 1149
Sequence: 1 CAAGCCCAGAGCCCTGCCAT............TCACCCCCCTCCTCCTCCTT 1149

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Searched: Gapop 10.0 , Gapext 1.0
4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Search time 4848.84 Seconds (without alignments)
11205.958 Million cell updates/sec

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        2: gb_htg:*
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        4: gb_om:*
        5: gb_ov:*
        6: gb_pat:*
        7: gb_ph:*
        8: gb_pl:*
        9: gb_pr:*
       10: gb_ro:*
       11: gb_sts:*
       12: gb_sy:*
       13: gb_un:*
       14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1149	100.0	1149	6	I08673	I08673 Sequence
4	1149	100.0	1149	6	AR130197	AR130197 Sequence
5	1149	100.0	1149	6	AR184213	AR184213 Sequence
6	1149	100.0	1149	6	AR229603	AR229603 Sequence
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13	687	59.8	1742	9	AX287109	AX287109 Sequence
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15	687	59.8	1796	6	HUMATCT4A	HUMATCT4A
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21	685.4	59.7	1742	6	AR104143	AR104143 Sequence
22	685.4	59.7	1742	6	I08673	I08673 Sequence 2
23	685.4	59.7	1742	6	AR339862	AR339862 Sequence
24	685.4	59.7	1742	6	AR448985	AR448985 Sequence
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33	664	57.7	1213	6	I08116	I08116 Sequence 3
34	657	57.2	1910	6	I08115	I08115 Sequence 1
35	657	57.2	3133	6	AR067943	AR067943 Sequence
36	655.4	57.0	1304	6	AR166802	AR166802 Sequence
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39	655.4	57.0	2589	6	AR392157	AR392157 Sequence
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41	653.8	56.9	3064	6	I09237	I09237 Sequence 1
42	652.4	56.8	719	6	AR067944	AR067944 Sequence
43	652.4	56.8	719	6	AR166803	AR166803 Sequence
44	652.2	56.8	5566	6	I09269	I09269 Sequence 36
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ALIGNMENTS

RESULT 1
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LOCUS   AR100742   1149 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6083478.
ACCESSION   AR100742
VERSION   AR100742.1 GI:12811540
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1149)
  AUTHORS   Allaway,G.P. and Maddon,P.J.
  TITLE   Non-peptidyl moiety-conjugated CD4-gamma2 and CD4-IgG2
            Immunoconjugates, and uses thereof
  JOURNAL   Patent: US 6083478-A 5 04-JUL-2000;
FEATURES   Location/Qualifiers
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Best Local Similarity   100.0%;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION  Sequence 5 from patent US 6177549.
ACCESSION   AR125612
VERSION     AR125612.1  GI:14111674
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1149)
  AUTHORS   Maddon,P.J. and Allaway,G.P.
  TITLE     Non-peptidyl moiety-conjugated CD4-gamma2 and CD4-IgG2
            immunoconjugates, and uses thereof
  JOURNAL   Patent: US 6177549-A 5 23-JAN-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN
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Best Local Similarity 100.0%;  Pred. No. 3.2e-292;
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Qy  601 CTCCAGGATAGTAGTGGGCACCTGGACATGCCACTGTCTTGCGAGAACCAGAAGAAGGTGGAGTTC  660
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Qy  661 AAAATAGACACGTGGTGCTAGCTTTCACTGTGCGTCGCCACCATCTGTTCTTCATTCTTCCG  720
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Db  661 AAAATAGACACGTGGTGCTAGCTTTCACTGTGCGTCGCCACCATCTGTTCTTCATTCTTCCG  720

Qy  721 CCATCTGATGAGCAGTTGAAATCTGAAACTGCCTCGTTGTTGGTGCCTGCTGAATAACTTC  780
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Db  721 CCATCTGATGAGCAGTTGAAATCTGAAACTGCCTCGTTGTTGGTGCCTGCTGAATAACTTC  780

Qy  781 TATCCCAGAGAGGCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAATCGGGGTAACTCC  840
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Db  781 TATCCCAGAGAGGCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAATCGGGGTAACTCC  840

Qy  841 CAGGAGAGTGTCACAGACAGCAGGACAGCACCTACAGCGCTACAGCCTCCCAGTCAGCAGCCACCTG  900
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Db  841 CAGGAGAGTGTCACAGACAGCAGGACAGCACCTACAGCGCTACAGCCTCCCAGTCAGCAGCCACCTG  900
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Db  241 TCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTCTTAACTAAAGGTCCATCCAAG  300
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Qy  241 TCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTCTTAACTAAAGGTCCATCCAAG  300

Db  301 CTGAATGATCGCGGCTGACTCAAGAGAAGAGAGCCTTTGGGACCAAGAAACTTCCCCCTGATC  360
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Qy  301 CTGAATGATCGCGGCTGACTCAAGAGAAGAGAGCCTTTGGGACCAAGAAACTTCCCCCTGATC  360

Db  361 ATCAAGAAATCTTAAGATAGAAGACTTCAGATACTTCATTCGTGTGAAGTGGGACCAGAAG  420
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Qy  361 ATCAAGAAATCTTAAGATAGAAGACTTCAGATACTTCATTCGTGTGAAGTGGGACCAGAAG  420

Db  421 GAGGAGGTGCAAATTGCTAGTGTTCGGATTGACTGCGCCAACCACCGGCTTCAG  480
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Db  481 GGGCAGAGCCTGACCTTGGAGAGGCCCCCTGGGTAGTAGCCCTCAGTGCAAATGT  540
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Qy  481 GGGCAGAGCCTGACCTTGGAGAGGCCCCCTGGGTAGTAGCCCTCAGTGCAAATGT  540

Db  541 AGGAGTCCAAGGGGTAAAAACATACAGGGGGGGAAGAGACCCTCTCCGTGTCTCAGCTGGAG  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  541 AGGAGTCCAAGGGGTAAAAACATACAGGGGGGGAAGAGACCCTCTCCGTGTCTCAGCTGGAG  600

Db  601 CTCCAGGATAGTAGTGGGCACCTGGACATGCCACTGTCTTGCGAGAACCAGAAGAAGGTGGAGTTC  660
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Db  661 AAAATAGACACGTGGTGCTAGCTTTCACTGTGCGTCGCCACCATCTGTTCTTCATTCTTCCG  720
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Qy  841 CAGGAGAGTGTCACAGACAGCAGGACAGCACCTACAGCGCTACAGCCTCCCAGTCAGCAGCCACCTG  900

Db  901 ACGCTGAGCAGAAGCAGGACTACGGAGAAAACACAAAGTCTACGGCCTGGAAGTCACCCATCAG  960
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Qy  901 ACGCTGAGCAGAAGCAGGACTACGGAGAAAACACAAAGTCTACGGCCTGGAAGTCACCCATCAG  960

Db  961 GGCCTGAGCTTCGCCCGTCACAAAGAGCTTCAACACAGGGACGAGTGTTAGAGGGAGAAGTGC  1020
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Db 1021 CCCCACCTGCTCCTCAGTTCCAGCCTGACCCCTCCCCATCCTCTTGGCCTTGACCCTTTTT  1080
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Qy 1021 CCCCACCTGCTCCTCAGTTCCAGCCTGACCCCTCCCCATCCTCTTGGCCTTGACCCTTTTT  1080

Db 1081 TCCACAGGGGACACCTACCCCTATTGCGGTCTCCCAAGCTTCATCTTTCACTCACCCCTC  1140
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Qy 1081 TCCACAGGGGACACCTACCCCTATTGCGGTCTCCCAAGCTTCATCTTTCACTCACCCCTC  1140

Db 1141 CTCCTCCTT  1149
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Qy 1141 CTCCTCCTT  1149
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OM nucleic - nucleic search, using sw model

                              GenCore version 5.1.6
                              Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: February 1, 2005, 03:40:26 ; Search time 3662.81 Seconds
                              (without alignments)
                              11430.900 Million cell updates/sec

Title: US-08-485-163-6
Perfect score: 1149
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Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0
Searched: 32822875 seqs, 1821986590B residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
             1: gb_est1:*
             2: gb_est2:*
             3: gb_htc:*
             4: gb_est3:*
             5: gb_est4:*
             6: gb_est5:*
             7: gb_est6:*
             8: gb_gss1:*
             9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
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c 2	645.4	56.2	783	5	CD609192	56069991J
c 3	642.8	55.9	816	4	BI838409	630083373
4	633.4	55.1	801	4	BI822118	603039813
5	632	55.0	822	6	BX457159	BX457159
6	630.2	54.8	840	4	BI838893	630087279
7	623.4	54.3	791	4	BI819727	603041415
8	586.6	51.1	713	5	BX437619	BX437619
9	553.4	48.2	723	4	BI915265	60318431J
10	551.4	48.0	679	6	CD609191	56069991H
11	549	47.8	732	7	AU141298	AU141298
12	533.8	46.5	754	7	CO246446	AGENCOURT
13	533.4	46.4	710	6	CF125444	UI-HF-EL0
14	528.8	46.0	694	6	CB052686	NISC_g109
15	525.6	45.7	803	7	CO249540	AGENCOURT
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17	497.8	43.3	821	7	CO245985	AGENCOURT
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19	453.6	39.5	809	7	CO248894	AGENCOURT
c 20	453	39.4	640	5	BU679704	UI-CF-EC1
21	452.6	39.4	751	7	CO248544	AGENCOURT
c 22	451.8	39.3	641	5	BQ062789	AGENCOURT
23	451.4	39.3	555	3	CR595815	full-leng
c 24	451.4	39.3	555	4	BI711498	id97e11.x
c 25	451.4	39.3	583	5	BU682271	UI-CF-EC1
c 26	451.4	39.3	593	5	CB985747	AGENCOURT
c 27	451.4	39.3	611	6	CA413070	UI-H-EL0-
c 28	451.4	39.3	620	4	BM511892	ij75d09.x
c 29	451.4	39.3	643	6	CA412343	UI-H-E20-
c 30	451.4	39.3	648	5	BM974791	UI-CF-EC1
c 31	451.4	39.3	692	6	CA447921	UI-H-EI0-
c 32	451.4	39.3	712	5	BU616742	UI-H-DF0-
c 33	451.4	39.3	731	5	BQ181514	UI-H-EU0-
c 34	451.4	39.3	776	5	BQ008671	UI-H-EI0-
c 35	451.4	39.3	798	5	BQ008761	UI-H-EI0-
c 36	450.6	39.2	536	6	BQ958453	AGENCOURT
c 37	450.4	39.2	566	4	BI765045	630511192
c 38	450.4	39.2	595	6	CB958067	AGENCOURT
c 39	450.4	39.2	603	6	CB957083	AGENCOURT
c 40	450.4	39.2	606	6	CB957335	AGENCOURT
c 41	450.4	39.2	643	5	BQ712156	UI-H-E10-
c 42	450.4	39.2	927	5	BQ706352	AGENCOURT
c 43	450.2	39.2	714	6	CA411822	AGENCOURT
c 44	450	39.2	521	6	CB956541	AGENCOURT
c 45	450	39.2	527	1	AJ708624	AJ708624

ALIGNMENTS

RESULT 1
BX438745
LOCUS   BX438745   932 bp   mRNA   linear   EST 05-MAY-2004
DEFINITION BX438745 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE002YG01
            5-PRIME, mRNA sequence.
ACCESSION   BX438745
VERSION   BX438745.2 GI:47035651
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 932)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30787731.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: Segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 6485.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DE002AD01QP1&c=6485.r.
FEATURES   Location/Qualifiers
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                    /clone_lib="Homo sapiens PLACENTA"
                    /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                    with a NotI-oligo(dT) primer. Five prime end enriched,
                    double-strand cDNA was digested with Not I and cloned into
                    the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                    Library was not normalized."
ORIGIN

Query Match 57.0%; Score 655.4; DB 5; Length 932;
Best Local Similarity 98.1%;
Matches 674; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

Left column

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Qy    11 GCCCTGCCANTTCTGTGGGCTCAGGTCCCTACTGCTC--AGCCCTTCTCCCCTCGGCGCAA   68
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Db   113 GCCCTGCCATTTCTGTGGGGGCTCAGGTCCCTACTGGCTCCAGCCCTTCTCCCCTGGGCGCT  172

Qy    69 GGGCCACAATGAAACCCGGGGGAGTCCCTTTTAGGCACTTGCTTCTGCTGTGTCGCAACTGGGCGCT  128
         |||||||||||||||||||| |||||||||||||||||||||||||||||||
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Qy   129 CCTCCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGGCAAAAAAAAGGGGATACAGTGGA  188
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Qy   189 ACTGACCTGTACAGCTTCCCAGAGAGAGAGGACATTACAATTCCACTGGAAAAAAACTCCAACCA  248
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Db   293 ACTGACCTGTACAGCTTCCCAGAGAGAGAGGACATTACAATTCCACTGGAAAAAAACTCCAACCA  352

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Db   353 GATAAAAGATTCTGGGAAAATCAGGGGCTCCTTCTTCTTAACTAAAGGTCCATCCAAGCTGAAATGA  412

Qy   309 TCGCCCTGACTCAAGGAAGGAAGCCCTTTGGGACCAAGGAAAACTTCCCCGTGATCATCAAGAA  368
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Db   413 TCGGCCTGACTCAAGGAAGGAAGCCCTTTGGGACCAAGGAAAACTTCCCCGTGATCATCAAGAA  472

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Db   473 TCTTAAGATAGAAGACTCAGATACTTACACTGTGTGAAGTGGAGGACCAGAGGAGGAGGT  532

Qy   429 GCAATTGCTAGTGTTCGGATTGACTGGGGTCCTCCTTCTTCTTAACTAAAGCTGAGGCAGAG  488
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Qy   489 CCTGACCCTGGAGAGCCCCCCCCTCGGTAGTGAGCCCTCAGTGCAAGTGAGTAGAGGTCC  548
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Qy   609 TAGTGGGGCACCTGGACATGGACATGCAACTCGTCTTGCGAGAACCAGAAGGTGGAGTTCAAAATAGA  668
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Db   713 TAGTGGGCACCTGGACATGCAACTCGTCTTGCGAGAACCAGAAGGTGGAGTTCAAAATAGA  772

Qy   669 CATCGTGGTGCTAGCTTTCACTGTGTGGCACC  695
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Db   773 CATCGTGGTGCTAGCTTTCACTGTGTGGCAA  799
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Right column

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Query Match        56.2%;  Score 645.4; DB 6;  Length 783;
Best Local Similarity   98.1%;  Pred. No. 1.1e-168;
Matches 664; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

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Qy   199 ACAGCTTCCCAGAGAGAGAGGACATCAATTCCACTGGAAAAAAACTCCAACCAGATAAAAGATT  258
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Qy   259 CTGGGAAAATCAGGGGCTCCTTCTTCTTAACTAAAGGTCCATCCAAGCTGAAATGATCGGCCTGAC  318
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Qy   319 TCAAGGAAGGAAGCCCTTTGGGACCAAGGAAAACTTCCCCGTGATCATCAAGAATCTTAAGATA  378
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Qy   379 GAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAGGAGGAGGTGCAAATTGCTA  438
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Db   423 GAAGACTCAGATACTTACATCTGTGTGAAGTGGAGGACCAGAGGAGGAGGTGCAAATTGCTA  364

Qy   439 GTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCCAGAGGACCCTG  498
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Db   303 ACCTTGGAGAGCCCCCCCCTCAGTGCGTAGTAGCCCTCAGTGCAAATGCAAGTGAGTCCAAGGGGTAAA  244

Qy   559 AACATACAGGGGGGGGAAGAACCCTCTCCGGTGTCTCAGCTGGAGCTTCCAGGATAGTGGCACC  618
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Db   243 AACATACAGGGGGGGGAAGAACCCTCTCCGGTGTCTCAGCTGGAGCTTCCAGGATAGTGGCACC  184

Qy   619 TGGACATGCACTGTCTTGCGAGAACCAGAAGGTGGAGTTCAAAATAGACATCGTGGTG  678
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Db   183 TGGACATGCACTGTCTTGCAGAACCAGAAGGTGGAGTTCAAAATAGACATCGTGGTG  124

Qy   679 CTAGCTTTCACTGTGTGGC  695
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Db   123 CTAGCTTTCACTGTGTGGC  107
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: February 1, 2005, 00:31:21 ; Search time 553.457 Seconds
                                             (without alignments)
                                             10898.026 Million cell updates/sec

Title: US-08-485-163-6
Perfect score: 1149
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Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 2: geneseqn1990s:*
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                 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149	100.0	1149	2	AAQ28090	Aaq28090 Encodes C
2	1149	100.0	1149	3	AAZ98857	Aaz98857 CD4-kappa
3	1149	100.0	1149	4	AAF56397	Aaf56397 CD4-kappa
4	1149	100.0	1149	10	AAF77831	Aaf77831 Coding se
5	1149	100.0	1149	11	ABS55722	Abs55722 DNA encod
6	1149	100.0	1149	10	ADM18323	Adm18323 Human CD4
7	1149	100.0	1149	2	AAQ57752	Aaq57752 CD4-kappa
8	1147.4	99.9	1149	2	AAQ27832	Aaq27832 Sequence
9	1147	99.8	1149	10	ACH00964	Ach00964 Pro 542 a
10	1107	96.3	11228	10	ACH00965	Ach00965 Pro 542 a
11	1062	92.4	3273	10	AAQ27831	Aaq27831 Sequence
12	698.4	60.8	2488	2	AAQ28089	Aaq28089 Encodes C
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15	696.8	60.6	2482	10	AAF77830	Aaf77830 Coding se
16	696.8	60.6	2482	11	ABS55721	Abs55721 DNA encod
17	696.8	60.6	2482	11	ADM18321	Adm18321 Human CD4
18	693.6	60.4	2482	2	AAQ57751	Aaq57751 CD4-IgG2
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21	687	59.8	1448	2	AAQ38759	Aaq38759 sCD4-HAP
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23	687	59.8	1742	2	AAF21327	Aaf21327 Human low
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25	687	59.8	1742	10	ABZ97021	Abz97021 Human nuc
26	687	59.8	1742	11	ADI31687	Adi31687 Human cDN
27	687	59.8	1742	11	ABD20870	Abd20870 Human pul
28	687	59.8	1796	2	AAQ28088	Aaq28088 Encodes C
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30	687	59.8	1796	3	AAZ98855	Aaz98855 Human CD4
31	687	59.8	1796	4	AAF56395	Aaf56395 CD4-gamma
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42	685.4	59.7	1742	3	AAA59352	Aaa59352 DNA encod
43	685.4	59.7	2465	2	AAQ38758	Aaq38758 sCD4-PCaD
44	683.8	59.5	2465	1	AAN90763	Aan90763 cDNA sequ
45	683.8	59.5	1273	3	AAA10906	Aaa10906 T4 glycop

ALIGNMENTS

RESULT 1
AAQ28090
ID   AAQ28090 standard; DNA; 1149 BP.
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AC   AAQ28090;
XX
DT   24-OCT-2003 (revised)
DT   25-MAR-2003 (revised)
DT   06-FEB-1993 (first entry)
XX
DE   Encodes CD4-IgG2 chimeric light chain.
XX
KW   homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW   chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key   Location/Qualifiers
FT   CDS   76..687
FT   /tag= a*
FT   /label= CD4 domain
FT   CDS   688..1005
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XX
PN   WO9213947-A1.
XX
PD   20-AUG-1992.
XX
PF   10-FEB-1992; 92WO-US001143.
XX
PR   08-FEB-1991; 91US-00653684.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Beaudry GA, Maddon PJ;
XX
DR   WPI; 1992-300034/36.
DR   P-PSDB; AAR26784.
XX
PT   CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT   treatment, prevention and diagnosis of HIV infection.
XX

PS   Claim 14; Fig 5; 90pp; English.
XX
CC   This sequence encodes a CD4-kappa chimeric light chain. Human kappa light
CC   chain constant region encoding sequence was excised from the plasmid
CC   pCNkappa light as an MseI fragment. This was blunt ended and ligated to
CC   M13mp18 at the HincII site. After transforming TGi cells the recombinants
CC   are screened by restriction analysis for the presence and correct
CC   orientation of the insert. Rf DNA is then isolated, and the purified
CC   vector then ligated to the EcoRI/StuI fragment of human CD4 cDNA. The
CC   resulting recombinants are then verified by the presence and orientation
CC   of both inserts containing in tandem CD4(EcoRI/StuI)-
CC   Ckappa(MseI(flush)/MseI(flush)). Site directed mutagenesis is then
CC   performed with an oligonucleotide containing sequences which join the
CC   last codon encoding Phe(179) from V1V2 of CD4 to the first codon of the
CC   kappa light chain constant domain (encoding Thr). (Updated on 25-MAR-2003
CC   to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1149 BP; 294 A; 337 C; 282 G; 236 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1149;   DB 2;   Length 1149;
Best Local Similarity   100.0%;   Pred No. 6.7e-301;
Matches 1149;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Db        1 CAAGCCCAGAGCCCTGCCCATTTCTGTGGGGCTCAGGGTCTCCCTACTGCTGCTCAGCCCTCCTCC   60

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Qy      241 TCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTTCCATCCAAG  300
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Qy      301 CTGAATGATGGCGCTGACTCAAGGAAGAAGCTTTTGGGACAAAGCTTCCCCTGATC  360
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Db      301 CTGAATGATGGCGCTGACTCAAGGAAGAAGCTTTTGGGACAAAGCTTCCCCTGATC  360

Qy      361 ATCAAGAAATCTTAAGATAGAAGAAGACTTACATTACATTGTGAAGTGGAGGACCAGAAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATCAAGAAATCTTAAGATAGAAGAAGACTTACATTACATTGTGAAGTGGAGGACCAGAAG  420

Qy      421 GAGGAGGTGCAATTGCTAGTGTTCGGATTGACTCGAACTCTGACACCCACCTGCTTCAG  480
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Db      421 GAGGAGGTGCAATTGCTAGTGTTCGGATTGACTCGAACTCTGACACCCACCTGCTTCAG  480

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Qy      661 AAAATAGACACTGGTAGTGCTAGCTTTCACTGTGGGCTGCACCATCTGTCTTCATCTTTCCCG  720
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Db      661 AAAATAGACACTGGTAGTGCTAGCTTTCACTGTGGGCTGCACCATCTGTCTTCATCTTTCCCG  720

Qy      721 CCATCTGATGAGCAGTTGAAATCTGAACTCCCTCTGTTGTGTGCCTGCTGAATAACTTC  780
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Db      721 CCATCTGATGAGCAGTTGAAATCTGAACTCCCTCTGTTGTGTGCCTGCTGAATAACTTC  780

Qy      841 CAGGAGAGTGTCACAGAGAGCAGGAGACAACAGGACTCAGCAGCTCAGCAGCACCCTG  900
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Qy      901 ACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGTCTACGGCTGCGAAGTCACCCATCAG  960
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Qy     1141 CTCCTCCTT 1149
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RESULT 2
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ID   AAZ98857 standard; DNA; 1149 BP.
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AC   AAZ98857;
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DT   19-JUN-2000   (first entry)
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DE   CD4-kappa chimeric light chain nucleotide sequence.
XX
KW   CD4-kappa chimeric light chain; immunoconjugate; treatment; CD4-IgG2;
KW   cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
KW   cellular immune response interaction mediator; HIV interaction; staging;
KW   prognosis; envelope glycoprotein burden; human; ds.
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XX
PN   US6034223-A.
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PD   07-MAR-2000.
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PF   07-JUN-1995;   95US-00477460.
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PR   07-AUG-1992;   92US-00927931.
PR   06-AUG-1993;   93WO-US007422.
PR   03-FEB-1995;   95US-00379516.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Allaway GP; Maddon PJ;
XX
DR   WPI; 2000-269502/23.
DR   P-PSDB; AAY85018.
XX
PT   New immunoconjugate, used to treat, prevent or image human immune
PT   deficiency virus infection, comprises radionuclide attached to
PT   heterotetramer of CD4-immunoglobulin chimeras.
XX
PS   Disclosure; Fig 5; 58pp; English.
XX
CC   This sequence represents the CD4-kappa chimeric light chain nucleotide
CC   sequence of the CD4-IgG2 chimeric heterotetramer. The invention relates

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: February 1, 2005, 09:02:41 ; Search time 620.542 Seconds
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SUMMARIES

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and is derived by analysis of the total score distribution.

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5	696.8	60.6	2482	8	US-08-485-163-4	Sequence 4, Appli
6	696.8	60.6	2482	9	US-09-766-995-3	Sequence 3, Appli
7	687	59.8	1742	14	US-10-151-274-7	Sequence 7, Appli
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11	685.4	59.7	1742	11	US-09-891-119A-8	Sequence 8, Appli
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17	655.4	57.0	1304	10	US-09-939-537-28	Sequence 28, Appl
18	655.4	57.0	3084	15	US-10-207-655-169	Sequence 169, App
19	652.4	56.8	719	10	US-09-939-537-30	Sequence 30, Appl
20	612	53.3	617	10	US-09-939-537-130	Sequence 7, Appli
21	612	53.3	1377	14	US-10-493-676-7	Sequence 38, Appl
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25	610.4	53.1	1389	11	US-09-243-008-2	Sequence 2, Appli
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30	610	53.1	1350	18	US-10-493-676-10	Sequence 10, Appl
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35	539.8	47.0	1508	15	US-10-097-044A-5	Sequence 5, Appli
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37	539	46.9	2379	14	US-10-073-118-24	Sequence 24, Appl
38	538	46.8	563	14	US-10-073-118-25	Sequence 25, Appl
39	537	46.7	1113	9	US-09-759-841-5	Sequence 5, Appli
40	534	46.5	534	9	US-09-934-060A-25	Sequence 25, Appl
41	534	46.5	1769	9	US-09-934-060A-12	Sequence 12, Appl
42	534	46.5	2159	9	US-09-934-060A-1	Sequence 1, Appli
43	534	46.5	2159	9	US-09-934-060A-3	Sequence 3, Appli
44	452.2	39.4	928	15	US-09-221-945-5	Sequence 5, Appli
45	451.4	39.3	913	9	US-09-822-830A-531	Sequence 531, App

ALIGNMENTS

RESULT 1
US-08-485-163-6

Sequence 6, Application US/08485163
; Publication No. US2002009819A1
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,163
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 1149 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
;   ORGANISM: homo sapien
;   CELL TYPE: lymphocyte
US-08-485-163-6

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RESULT 2
US-09-766-995-5
; Sequence 5, Application US/09766995
; Patent No. US20020052481A1
; GENERAL INFORMATION:
;   APPLICANT: Graham P. Allaway et al.
;   TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJU
;   TITLE OF INVENTION:  AND USES THEREOF
;   FILE REFERENCE: 2048/41215-CB/JPW/SHS
;   CURRENT APPLICATION NUMBER: US/09/766,995
;   CURRENT FILING DATE:  2001-01-22
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: Patentin version 3.0
SEQ ID NO 5
;   LENGTH: 1149
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-766-995-5

Query Match             100.0%;  Score 1149;  DB 9;  Length 1149;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1149;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy    121 CTGGGCGCTCCTCCCAGCAGCCACTCAGGGGAAAGAAAGTGGTCGGGCAA 180
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Qy    301 CTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAAGGAAAACTTCCCCCTGATC 360
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Qy    361 ATCAAGAAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAG 420
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Db    361 ATCAAGAAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAG 420
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: February 1, 2005, 03:49:56 ; Search time 98.0969 Seconds
                                         (without alignments)
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Title: US-08-485-163-6
Perfect score: 1149
Sequence: 1 CAAGCCCAGAGCCCTGCCAT..........TCACCCCCCTCCTCCTCCTT 1149
Scoring table: IDENTITY NUC
                Gapop 10.0 , Gapext 1.0
Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
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                Pred. No. is the number of results predicted by chance to have a
                score greater than or equal to the score of the result being printed,
                and is derived by analysis of the total score distribution.

SUMMARIES

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1	1149	100.0	1149	3	US-08-477-460B-5	Sequence 5, Appli
2	1149	100.0	1149	3	US-08-379-516-5	Sequence 5, Appli
3	1149	100.0	1149	3	US-09-329-916-5	Sequence 5, Appli
4	1149	100.0	1149	3	US-08-485-372A-5	Sequence 5, Appli
5	1149	100.0	1149	3	US-09-409-006A-5	Sequence 5, Appli
6	1149	100.0	1149	4	US-08-484-681-5	Sequence 5, Appli
7	1149	100.0	1149	5	US-09-766-995-5	Sequence 5, Appli
8	1149	100.0	1149	5	PCT-US93-07422-5	Sequence 5, Appli
9	696.8	60.6	2482	3	US-08-477-460B-3	Sequence 3, Appli
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13	696.8	60.6	2482	3	US-09-409-006A-3	Sequence 3, Appli
14	696.8	60.6	2482	4	US-08-484-681-3	Sequence 3, Appli
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17	687	59.8	1415	5	PCT-US92-08090-4	Sequence 4, Appli
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19	687	59.8	1448	5	PCT-US92-08090-2	Sequence 2, Appli
20	687	59.8	1742	4	US-09-517-605-7	Sequence 7, Appli
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26	687	59.8	1796	3	US-09-409-006A-1	Sequence 1, Appli
27	687	59.8	1796	4	US-08-484-681-1	Sequence 1, Appli
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33	685.4	59.7	1742	4	US-08-328-500-8	Sequence 8, Appli
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35	683.8	59.5	1273	4	US-08-328-500-1	Sequence 1, Appli
36	683.8	59.5	1416	1	US-08-236-311-2	Sequence 2, Appli
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40	655.4	57.0	1304	2	US-08-284-391B-28	Sequence 28, Appl
41	655.4	57.0	1304	3	US-09-218-950-28	Sequence 28, Appl
42	655.4	57.0	1304	4	US-08-394-388A-28	Sequence 28, Appl
43	655.4	57.0	2589	4	US-08-472-888A-5	Sequence 5, Appli
44	652.4	56.8	719	2	US-08-284-391B-30	Sequence 30, Appl
45	652.4	56.8	719	3	US-09-218-950-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-477-460B-5
; Sequence 5, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,460B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte

US-08-477-460B-5

Query Match   100.0%; Score 1149; DB 3; Length 1149;
Best Local Similarity   100.0%; Pred. No. 0;

Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 CAAGCCCAGAGACCCTGCCATTTCTGTGGGCTCAGTCTCAGTCTCAGCCCTTCCTCC   60

Qy     61 CTCGGCAAGGCCACAATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCAA  120
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Db    121 CTGGGCCTCCTCCCAGCAGCCACTCAGGGGAAAGAAAAGTGGTTGCTGGGCAAAAAGGGGAT  180

Qy    181 ACAGTGGGACTGACCTGTACAGCTTCCCAGAAGAGAGCATACAAATTCCACTGGGAAAAC  240
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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